



1600

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/762,261B

DATE: 01/09/2003
TIME: 11:45:42

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JAN 21 2003

TECH CENTER 1600/2900

Input Set : A:\Hj5001u1.app
Output Set: N:\CRF4\01092003\I762261B.raw

3 <110> APPLICANT: Quinnan, Gerald V.
4 Zhang, Peng Fei
6 <120> TITLE OF INVENTION: Expression and Characterization of HIV-1 Envelope
7 Protein Associated with a Broadly Reactive Neutralizing
8 Antibody Response
10 <130> FILE REFERENCE: 44508-5001-US
12 <140> CURRENT APPLICATION NUMBER: US 09/762,261B
C--> 13 <141> CURRENT FILING DATE: 2001-05-29
15 <150> PRIOR APPLICATION NUMBER: US 60/095,267
16 <151> PRIOR FILING DATE: 1998-08-04
18 <150> PRIOR APPLICATION NUMBER: PCT/US99/17596
19 <151> PRIOR FILING DATE: 1999-08-04
21 <160> NUMBER OF SEQ ID NOS: 23
23 <170> SOFTWARE: PatentIn Ver. 2.1
25 <210> SEQ ID NO: 1
26 <211> LENGTH: 866
27 <212> TYPE: PRT
28 <213> ORGANISM: Human immunodeficiency virus type 1
30 <220> FEATURE:
31 <223> OTHER INFORMATION: R2 strain envelope protein (gp 160)
33 <400> SEQUENCE: 1
34 Met Arg Val Lys Gly Ile Arg Arg Asn Tyr Gln His Trp Trp Gly Trp
35 1 5 10 15
37 Gly Thr Met Leu Leu Gly Leu Leu Met Ile Cys Ser Ala Thr Glu Lys
38 20 25 30
40 Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp Lys Glu Ala Thr
41 35 40 45
43 Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr Asp Thr Glu Ala
44 50 55 60
46 His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro Asn Pro
47 65 70 75 80
49 Gln Glu Val Glu Leu Val Asn Val Thr Glu Asn Phe Asn Met Trp Lys
50 85 90 95
52 Asn Asn Met Val Glu Gln Met His Glu Asp Ile Ile Ser Leu Trp Asp
53 100 105 110
55 Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Thr Leu
56 115 120 125
58 Asn Cys Thr Asp Leu Arg Asn Thr Thr Asn Thr Asn Asn Ser Thr Asp
59 130 135 140
61 Asn Asn Asn Ser Asn Ser Glu Gly Thr Ile Lys Gly Gly Glu Met Lys
62 145 150 155 160
64 Asn Cys Ser Phe Asn Ile Ala Thr Ser Ile Gly Asp Lys Met Gln Lys
65 165 170 175

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67 Glu Tyr Ala Leu Leu Tyr Lys Leu Asp Ile Glu Pro Ile Asp Asn Asp
 68 180 185 190
 70 Asn Thr Ser Tyr Arg Leu Ile Ser Cys Asn Thr Ser Val Ile Thr Gln
 71 195 200 205
 73 Ala Cys Pro Lys Ile Ser Phe Glu Pro Ile Pro Ile His Tyr Cys Ala
 74 210 215 220
 76 Pro Ala Gly Phe Ala Ile Leu Lys Cys Asn Asp Lys Lys Phe Ser Gly
 77 225 230 235 240
 79 Lys Gly Ser Cys Lys Asn Val Ser Thr Val Gln Cys Thr His Gly Ile
 80 245 250 255
 82 Arg Pro Val Val Ser Thr Gln Leu Leu Leu Asn Gly Ser Leu Ala Glu
 83 260 265 270
 85 Glu Glu Val Val Ile Arg Ser Glu Asn Phe Thr Asn Asn Ala Lys Thr
 86 275 280 285
 88 Ile Ile Val Gln Leu Arg Glu Pro Val Lys Ile Asn Cys Ser Arg Pro
 89 290 295 300
 91 Asn Asn Asn Thr Arg Lys Ser Ile Pro Met Gly Pro Gly Arg Ala Phe
 92 305 310 315 320
 94 Tyr Thr Thr Gly Gln Ile Ile Gly Asp Ile Arg Gln Ala His Cys Asn
 95 325 330 335
 97 Ile Ser Lys Thr Asn Trp Thr Asn Ala Leu Lys Gln Val Val Glu Lys
 98 340 345 350
 100 Leu Gly Glu Gln Phe Asn Lys Thr Lys Ile Val Phe Thr Asn Ser Ser
 101 355 360 365
 103 Gly Gly Asp Pro Glu Ile Val Thr His Ser Phe Asn Cys Ala Gly Glu
 104 370 375 380
 106 Phe Phe Tyr Cys Asn Thr Thr Gln Leu Phe Asp Ser Ile Trp Asn Ser
 107 385 390 395 400
 109 Glu Asn Gly Thr Trp Asn Ile Thr Arg Gly Leu Asn Asn Thr Gly Arg
 110 405 410 415
 112 Asn Asp Thr Ile Thr Leu Pro Cys Arg Ile Lys Gln Ile Ile Asn Arg
 113 420 425 430
 115 Trp Gln Glu Val Gly Lys Ala Met Tyr Ala Pro Pro Ile Lys Gly Asn
 116 435 440 445
 118 Ile Ser Cys Ser Ser Asn Ile Thr Gly Leu Leu Leu Thr Arg Asp Gly
 119 450 455 460
 121 Gly Lys Asp Asp Asn Ser Arg Asp Gly Asn Glu Thr Phe Arg Pro Gly
 122 465 470 475 480
 124 Gly Gly Asp Met Arg Asp Asn Trp Arg Ser Glu Leu Tyr Lys Tyr Lys
 125 485 490 495
 127 Val Val Lys Ile Glu Pro Leu Gly Val Ala Pro Thr Lys Ala Lys Arg
 128 500 505 510
 130 Arg Val Val Gln Arg Glu Glu Arg Ala Val Gly Leu Gly Ala Met Phe
 131 515 520 525
 133 Phe Gly Phe Leu Gly Ala Ala Gly Ser Thr Met Gly Ala Ala Ser Val
 134 530 535 540
 136 Thr Leu Thr Val Gln Ala Arg Gln Leu Leu Ser Gly Ile Val Gln Gln
 137 545 550 555 560
 139 Gln Ser Asn Leu Leu Arg Ala Ile Glu Ala Gln Gln His Leu Leu Gln

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140                                     565                                     570                                     575
142 Leu Thr Val Trp Gly Ile Lys Gln Leu Gln Ala Arg Ile Leu Ala Val
143                                     580                                     585                                     590
145 Glu Arg Tyr Leu Lys Asp Gln Gln Leu Leu Gly Ile Trp Gly Cys Ser
146                                     595                                     600                                     605
148 Gly Lys Leu Ile Cys Thr Thr Thr Val Pro Trp Asn Ala Ser Trp Ser
149                                     610                                     615                                     620
151 Lys Asn Lys Thr Leu Glu Ala Ile Trp Asn Asn Met Thr Trp Met Gln
152 625                                     630                                     635                                     640
154 Trp Asp Lys Glu Ile Asp Asn Tyr Thr Ser Leu Ile Tyr Ser Leu Ile
155                                     645                                     650                                     655
157 Glu Glu Ser Pro Ile Gln Gln Glu Lys Asn Glu Gln Glu Leu Glu
158                                     660                                     665                                     670
160 Leu Asp Lys Trp Ala Asn Leu Trp Asn Trp Phe Asp Ile Ser Asn Trp
161                                     675                                     680                                     685
163 Leu Trp Tyr Ile Lys Ile Phe Ile Met Ile Val Gly Gly Leu Val Gly
164                                     690                                     695                                     700
166 Leu Arg Ile Val Phe Val Val Leu Ser Ile Val Asn Arg Val Arg Gln
167 705                                     710                                     715                                     720
169 Gly Tyr Ser Pro Leu Ser Phe Gln Thr Arg Leu Pro Ala Pro Arg Gly
170                                     725                                     730                                     735
172 Pro Asp Arg Pro Glu Glu Ile Glu Glu Glu Gly Gly Asp Arg Asp Arg
173                                     740                                     745                                     750
175 Asp Arg Ser Gly Leu Leu Val Asp Gly Phe Leu Thr Leu Ile Trp Val
176                                     755                                     760                                     765
178 Asp Leu Arg Ser Leu Cys Leu Phe Ser Tyr His Arg Leu Arg Asp Leu
179                                     770                                     775                                     780
181 Leu Leu Ile Val Thr Arg Ile Val Glu Leu Leu Gly Arg Arg Gly Trp
182 785                                     790                                     795                                     800
184 Glu Ile Leu Lys Tyr Trp Trp Asn Leu Leu Gln Tyr Trp Ser Gln Glu
185                                     805                                     810                                     815
187 Leu Lys Asn Ser Ala Val Ser Leu Phe Asn Ala Thr Ala Ile Ala Val
188                                     820                                     825                                     830
190 Ala Glu Gly Thr Asp Arg Val Ile Gln Val Leu Gln Arg Val Gly Arg
191                                     835                                     840                                     845
193 Ala Leu Leu His Ile Pro Thr Arg Ile Arg Gln Gly Leu Glu Arg Ala
194                                     850                                     855                                     860
196 Leu Leu
197 865
200 <210> SEQ ID NO: 2
201 <211> LENGTH: 17
202 <212> TYPE: PRT
203 <213> ORGANISM: Human immunodeficiency virus type 1
205 <220> FEATURE:
206 <223> OTHER INFORMATION: segment of R2 strain V3 domain
208 <400> SEQUENCE: 2
209 Lys Ser Ile Pro Met Gly Pro Gly Arg Ala Phe Tyr Thr Thr Gly Gln
210 1                                     5                                     10                                     15
212 Ile

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216 <210> SEQ ID NO: 3
217 <211> LENGTH: 35
218 <212> TYPE: PRT
219 <213> ORGANISM: Human immunodeficiency virus type 1
221 <220> FEATURE:
222 <223> OTHER INFORMATION: R2 strain V3 domain
224 <400> SEQUENCE: 3
225 Cys Ser Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile Pro Met Gly Pro
226 1 5 10 15
228 Gly Arg Ala Phe Tyr Thr Thr Gly Gln Ile Ile Gly Asp Ile Arg Gln
229 20 25 30
231 Ala His Cys
232 35
235 <210> SEQ ID NO: 4
236 <211> LENGTH: 35
237 <212> TYPE: PRT
238 <213> ORGANISM: Human immunodeficiency virus type 1
240 <220> FEATURE:
241 <223> OTHER INFORMATION: V3 domain of strain 93TH966.8
243 <400> SEQUENCE: 4
244 Cys Thr Arg Pro Ser Asn Asn Thr Arg Thr Ser Thr Thr Ile Gly Pro
245 1 5 10 15
247 Gly Gln Val Phe Tyr Arg Thr Gly Asp Ile Thr Gly Asn Ile Arg Lys
248 20 25 30
250 Ala Tyr Cys
251 35
254 <210> SEQ ID NO: 5
255 <211> LENGTH: 13
256 <212> TYPE: PRT
257 <213> ORGANISM: Artificial Sequence
259 <220> FEATURE:
260 <223> OTHER INFORMATION: Description of Artificial Sequence: derivatives
261 of segment of V3 domain in R2 strain
263 <220> FEATURE:
264 <221> NAME/KEY: VARIANT
265 <222> LOCATION: (3)..(12)
266 <223> OTHER INFORMATION: X = any natural or non-natural amino acid.
268 <400> SEQUENCE: 5
W--> 269 Pro Met Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Gln
270 1 5 10
273 <210> SEQ ID NO: 6
274 <211> LENGTH: 30
275 <212> TYPE: PRT
276 <213> ORGANISM: Human immunodeficiency virus type 1
278 <220> FEATURE:
279 <223> OTHER INFORMATION: sequence of Phenetic 1 in V3 region
281 <400> SEQUENCE: 6
282 Asn Asn Thr Arg Lys Ser Ile His Ile Gly Pro Gly Arg Ala Phe Tyr
283 1 5 10 15

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Input Set : A:\Hj5001u1.app
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285 Thr Thr Gly Asp Ile Ile Gly Asp Ile Arg Gln Ala His Cys
286 20 25 30
289 <210> SEQ ID NO: 7
290 <211> LENGTH: 30
291 <212> TYPE: PRT
292 <213> ORGANISM: Human immunodeficiency virus type 1
294 <220> FEATURE:
295 <223> OTHER INFORMATION: sequence of Phenetic 2 in V3 region
297 <400> SEQUENCE: 7
298 Asn Asn Thr Arg Lys Ser Ile Ser Ile Gly Pro Gly Arg Ala Phe Tyr
299 1 5 10 15
301 Ala Thr Gly Glu Ile Ile Gly Asp Ile Arg Gln Ala His Cys
302 20 25 30
305 <210> SEQ ID NO: 8
306 <211> LENGTH: 30
307 <212> TYPE: PRT
308 <213> ORGANISM: Human immunodeficiency virus type 1
310 <220> FEATURE:
311 <223> OTHER INFORMATION: sequence of Phenetic 3 in V3 region
313 <400> SEQUENCE: 8
314 Asn Asn Thr Arg Lys Ser Ile Ser Ile Gly Pro Gly Arg Ala Phe Tyr
315 1 5 10 15
317 Ala Thr Gly Lys Ile Ile Gly Asp Ile Arg Gln Ala His Cys
318 20 25 30
321 <210> SEQ ID NO: 9
322 <211> LENGTH: 30
323 <212> TYPE: PRT
324 <213> ORGANISM: Human immunodeficiency virus type 1
326 <220> FEATURE:
327 <223> OTHER INFORMATION: sequence of Phenetic 4 in V3 region
329 <400> SEQUENCE: 9
330 Asn Asn Thr Arg Lys Ser Ile Arg Ile Gly Pro Gly Gln Ala Phe Tyr
331 1 5 10 15
333 Ala Thr Gly Asp Ile Ile Gly Asp Ile Arg Gln Ala His Cys
334 20 25 30
337 <210> SEQ ID NO: 10
338 <211> LENGTH: 30
339 <212> TYPE: PRT
340 <213> ORGANISM: Human immunodeficiency virus type 1
342 <220> FEATURE:
343 <223> OTHER INFORMATION: sequence of Phenetic 5 in V3 region
345 <400> SEQUENCE: 10
346 Asn Asn Thr Arg Lys Ser Ile His Ile Gly Pro Gly Arg Ala Phe Tyr
347 1 5 10 15
349 Ala Thr Gly Lys Ile Ile Gly Asp Ile Arg Gln Ala His Cys
350 20 25 30
353 <210> SEQ ID NO: 11
354 <211> LENGTH: 30
355 <212> TYPE: PRT

RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/09/762,261B

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:5; Xaa Pos. 3,4,5,6,7,8,9,10,11,12

1/9/03